IN THE SPECIFICATION:

On page 7, please amend the paragraph beginning at line 21 as follows:

Figure 3, comprising Figures 3A through 3S, depicts an alignment of the nucleotide sequence of a cDNA encoding human 22437 protein described herein ("22437"; SEQ ID NO: 1) and the nucleotide sequence of a cDNA encoding human KIAA1427 ("1427"; SEQ ID NO: 11). The alignment was made using the ALIGN software available at [[http://]]xyliam.igh.cnrs.fr/bin/nph-align_query.pl, using the default parameters, including gap opening penalty = 12, and gap extension penalty = 2 (Parson et al., 1997, Genomics 46:24-36).

On page 8, please amend the paragraph beginning at line 26 as follows:

For general information regarding PFAM identifiers, PS prefix and PF prefix domain identification numbers, refer to Sonnhammer et al. (1997, Protein 28:405-420) and [[http://]]www.psc.edu/general/ software/packages/pfam/pfam.html.

On page 9, please amend the paragraph beginning at line 11 as follows:

A 22437 polypeptide can include a sulfatase domain. As used herein, the term "sulfatase domain" refers to a protein domain having an amino acid sequence about 300-500 residues in length, preferably, at least about 400-500 residues, more preferably about 429 residues and has a bit score for the alignment of the sequence to the sulfatase domain (HMM) of at least 100 or greater, preferably 200 or greater, and more preferably 250 or greater. The sulfatase domain has been assigned the PFAM accession PF00884 ([[http://]]genome.wustl.edu/Pfam/html).

On pages 9 and 10, please amend the paragraph beginning at line 23 of page 9 as follows:

To identify the presence of a sulfatase domain profile in a 22437 receptor, the amino acid sequence of the protein is searched against a database of HMMs (e.g., the Pfam database, release 2.1) using the default parameters ([[http://]]www.sanger.ac.uk/Software/Pfam/HMM_search). For example, the hmmsf program, which is available as part of the HMMER package of search programs, is a family specific default program for PF00884 and score of 100 is the default

threshold score for determining a hit. For example, using ORFAnalyzer software, a sulfatase domain profile was identified in the amino acid sequence of SEQ ID NO: 2 (e.g., amino acids 44-472 of SEQ ID NO: 2). Accordingly, a 22437 protein having at least about 60-70%, more preferably about 70-80%, or about 80-90% homology with the sulfatase domain profile of human 22437 is within the scope of the invention.

On pages 20 and 21, please amend the paragraph beginning at line 23 of page 20 as follows:

The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman et al. (1970, J. Mol. Biol. 48:444-453) algorithm which has been incorporated into the GAP program in the GCG software package (available at [[http://]]www.gcg.com), using either a BLOSUM 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (available at [[http://]]www.gcg.com), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. A particularly preferred set of parameters (and the one that should be used if the practitioner is uncertain about what parameters should be applied to determine if a molecule is within a sequence identity or homology limitation of the invention) are a BLOSUM 62 scoring matrix with a gap penalty of 12, a gap extend penalty of 4, and a frameshift gap penalty of 5.

On page 21, please amend the paragraph beginning at line 11 as follows:

The nucleic acid and protein sequences described herein can be used as a "query sequence" to perform a search against public databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, et al. (1990, J. Mol. Biol. 215:403-410). BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to 22437 nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to 22437 protein molecules of the invention. To obtain gapped alignments for comparison purposes, gapped BLAST can be utilized as described in Altschul et al. (1997, Nucl. Acids Res. 25:3389-3402). When using BLAST and gapped

BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See <[[http://]]www.ncbi.nlm.nih.gov>.